

RAW SEQUENCE LISTING
PATENT APPLICATION US/08/070,455DATE: 12/10/93
TIME: 11:58:59

INPUT SET: S2078.raw

SEQUENCE LISTING

ENTERED

- 1
2
3 (1) General Information:
4
5 (i) APPLICANT: HOFVANDER, Per
6 PERSSON, Per T
7 WIKSTROM, Olle
8 TALLBERG, Anneli
9
10 (ii) TITLE OF INVENTION: GENETICALLY ENGINEERED MODIFICATION OF
11 POTATO TO FORM AMYLOPECTIN-TYPE STARCH
12
13 (iii) NUMBER OF SEQUENCES: 21
14
15 (iv) CORRESPONDENCE ADDRESS:
16 (A) ADDRESSEE: Burns, Doane, Swecker & Mathis
17 (B) STREET: George Mason Bldg., Washington & Prince Sts.
18 (C) CITY: Alexandria
19 (D) STATE: Virginia
20 (E) COUNTRY: United States
21 (F) ZIP: 22313-1404
22
23 (v) COMPUTER READABLE FORM:
24 (A) MEDIUM TYPE: Floppy disk
25 (B) COMPUTER: IBM PC compatible
26 (C) OPERATING SYSTEM: PC-DOS/MS-DOS
27 (D) SOFTWARE: PatentIn Release #1.0, Version #1.25
28
29 (vi) CURRENT APPLICATION DATA:
30 (A) APPLICATION NUMBER: US 08/070,455
31 (B) FILING DATE: 09-JUN-1993
32 (C) CLASSIFICATION:
33
34 (viii) ATTORNEY/AGENT INFORMATION:
35 (A) NAME: Crane-Feury, Sharon E
36 (B) REGISTRATION NUMBER: 36,113
37 (C) REFERENCE/DOCKET NUMBER: 003300-293
38
39 (ix) TELECOMMUNICATION INFORMATION:
40 (A) TELEPHONE: (703) 836-6620
41 (B) TELEFAX: (703) 836-2021
42
43
44 (2) INFORMATION FOR SEQ ID NO:1:
45
46 (i) SEQUENCE CHARACTERISTICS:
47 (A) LENGTH: 342 base pairs
48 (B) TYPE: nucleic acid
49 (C) STRANDEDNESS: double
50 (D) TOPOLOGY: linear
51

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52 (ii) MOLECULE TYPE: DNA (genomic)
53
54 (ix) FEATURE:
55 (A) NAME/KEY: CDS
56 (B) LOCATION: 217..342
57
58 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:
59
60 TGCATGTTTC CCTACATTCT ATTTAGAATC GTGTTGTGGT GTATAAACGT TGTTTCATAT 60
61
62 CTCATCTCAT CTATTCTGAT TTTGATTCTC TTGCCTACTG TAATCGGTGA TAAATGTGAA 120
63
64 TGCTTCCTTT CTTCTCAGAA ATCAATTTCT GTTTTGT TTTT TGTTTCATCTG TAGCTTATTC 180
65
66 TCTGGTAGAT TCCCCTTTTT GTAGACCACA CATCAC ATG GCA AGC ATC ACA GCT 234
67 Met Ala Ser Ile Thr Ala
68 1 5
69
70 TCA CAC CAC TTT GTG TCA AGA AGC CAA ACT TCA CTA GAC ACC AAA TCA 282
71 Ser His His Phe Val Ser Arg Ser Gln Thr Ser Leu Asp Thr Lys Ser
72 10 15 20
73
74 ACC TTG TCA CAG ATA GGA CTC AGG AAC CAT ACT CTG ACT CAC AAT GGT 330
75 Thr Leu Ser Gln Ile Gly Leu Arg Asn His Thr Leu Thr His Asn Gly
76 25 30 35
77
78 TTA AGG GCT GTT 342
79 Leu Arg Ala Val
80 40
81
82
83 (2) INFORMATION FOR SEQ ID NO:2:
84
85 (i) SEQUENCE CHARACTERISTICS:
86 (A) LENGTH: 2549 base pairs
87 (B) TYPE: nucleic acid
88 (C) STRANDEDNESS: single
89 (D) TOPOLOGY: linear
90
91 (ii) MOLECULE TYPE: DNA (genomic)
92
93 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:
94
95 AACAAAGCTTG ATGGGCTCCA ATCAACAACT AATACTAAGG TAACACCCAA GATGGCATCC 60
96
97 AGAACTGAGA CCAAGAGACC TGGATGCTCA GCTACCATTG TTTGTGGAAA GGAATGAAC 120
98
99 TTGATCTTTG TGGGTACTGA GGTGCTCCT TGGAGCAAAA CTGGTGGACT AGGTGATGTT 180
100
101 CTTGGTGGAC TACCACCAGC CCTTGCAGTA AGTCTTTCTT TCATTTGGTT ACCTACTCAT 240
102

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103	TCATTACTTA	TTTTGTTTAG	TTAGTTTCTA	CTGCATCAGT	CTTTTTATCA	TTTAGGCCCCG	300
104							
105	CGGACATCGG	GTAATGACAA	TATCCCCCGG	TTATGACCAA	TACAAAGATG	CTTGGGATAC	360
106							
107	TGGCGTTGCG	GTTGAGGTAC	ATCTTCCTAT	ATTGATACGG	TACAATATTG	TTCTCTTACA	420
108							
109	TTTCCTGATT	CAAGAATGTG	ATCATCTGCA	GGTCAAAGTT	GGAGACAGCA	TTGAAATTGT	480
110							
111	TCGTTTCTTT	CACTGCTATA	AACGTGGGGT	TGATCGTGTT	TTTGTTGACC	ACCCAATGTT	540
112							
113	CTTGAGAGAAA	GTAAGCATAT	TATGATTATG	AATCCGTCCT	GAGGGATACG	CAGAACAGGT	600
114							
115	CATTTTGAGT	ATCTTTTAAC	TCTACTGGTG	CTTTTACTCT	TTTAAGGTTT	GGGGCAAAAC	660
116							
117	TGGTTCAAAA	ATCTATGGCC	CCAAAGCTGG	ACTAGATTAT	CTGGACAATG	AACTTAGGTT	720
118							
119	CAGCTTGTTG	TGTCAAGTAA	GTTAGTTACT	CTTGATTTTT	ATGTGGCATT	TTACTCTTTT	780
120							
121	GTCTTTAATC	GTTTTTTTAA	CCTTGTTTTT	TCAGGCAGCC	CTAGAGGCAC	CTAAAGTTTT	840
122							
123	GAATTTGAAC	AGTAGCAACT	ACTTCTCAGG	ACCATATGGT	AATTAACACA	TCCTAGTTTC	900
124							
125	AGAAAACCTC	TTACTATATC	ATTGTAGGTA	ATCATCTTTA	TTTTGCCTAT	TCCTGCAGGA	960
126							
127	GAGGATGTTT	TCTTCATTGC	CAATGATTGG	CACACAGCTC	TCATTCCTTG	CTACTTGAAG	1020
128							
129	TCAATGTACC	AGTCCAGAGG	AATCTACTTG	AATGCCAAGG	TAAAATTTCT	TTGTATTAC	1080
130							
131	TCGATTGCAC	GTTACCCCTG	AAATCAGTAA	GGTTGTATTA	ATATATGATA	AATTTACAT	1140
132							
133	TGCCTCCAGG	TTGCTTTCTG	CATCCATAAC	ATTGCCTACC	AAGGTCGATT	TTCTTTCTCT	1200
134							
135	GACTTCCCTC	TTCTCAATCT	TCCTGATGAA	TTCAGGGGTT	CTTTTGATTT	CATTGATGGG	1260
136							
137	TATGTATTTA	TGCTTGAAAT	CAGACCTCCA	ACTTTTGAAG	CTCTTTTGAT	GCTAGTAAAT	1320
138							
139	TGAGTTTTTA	AAATTTTGCA	GATATGAGAA	GCCTGTAAAG	GGTAGGAAAA	TCAACTGGAT	1380
140							
141	GAAGGCTGGG	ATATTAGAAT	CACATAGGGT	GGTTACAGTG	AGCCCATACT	ATGCCCAAGA	1440
142							
143	ACTTGTCTCT	GCTGTTGACA	AGGGAGTTGA	ATTGGACAGT	GTCCTTCGTA	AGACTTGCAT	1500
144							
145	AACTGGGATT	GTGAATGGCA	TGGATACACA	AGAGTGGAAC	CCAGCGACTG	ACAAATACAC	1560
146							
147	AGATGTCAAA	TACGATATAA	CCACTGTAAG	ATAAGATTTT	TCCGACTCCA	GTATATACTA	1620
148							
149	AATTATTTTG	TATGTTTATG	AAATTAAAGA	GTTCTTGCTA	ATCAAAATCT	CTATACAGGT	1680
150							
151	CATGGACGCA	AAACCTTTAC	TAAAGGAGGC	TCTTCAAGCA	GCAGTTGGCT	TGCCTGTTGA	1740
152							
153	CAAGAAGATC	CCTTTGATTG	GCTTCATCGG	CAGACTTGAG	GAGCAGAAAAG	G TTCAGATAT	1800

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154
155 TCTTGTGCT GCAATTCACA AGTTCATCGG ATTGGATGTT CAAATTGTAG TCCTTGTAAG 1860
156
157 TACCAAATGG ACTCATGGTA TCTCTCTTGT TGAGTTTACT TGTGCCGAAA CTGAAATTGA 1920
158
159 CCTGCTACTC ATCCTATGCA TCAGGGAAGT GGCAAAAAGG AGTTTGAGCA GGAGATTGAA 1980
160
161 CAGCTCGAAG TGTGTACCC TAACAAAGCT AAAGGAGTGG CAAAATTCAA TGTCCCTTTG 2040
162
163 GCTCACATGA TCACTGCTGG TGCTGATTTT ATGTTGGTTC CAAGCAGATT TGAACCTTGT 2100
164
165 GGTCTCATTC AGTTACATGC TATGCGATAT GGAACAGTAA GAACCAGAAG AGCTTGTTACC 2160
166
167 TTTTACTGA GTTTTAAAA AAAGAATCAT AAGACCTTGT TTTCCATCTA AAGTTTAATA 2220
168
169 ACCAACTAAA TGTTACTGCA GCAAGCTTTT CATTTCTGAA AATTGGTTAT CTGATTTTAA 2280
170
171 CGTAATCACA TGTGAGTCAG GTACCAATCT GTGCATCGAC TGGTGGACTT GTTGACACTG 2340
172
173 TGAAAGAAGG CTATACTGGA TTCCATATGG GAGCCTTCAA TGTGAAGTA TGTGATTTTA 2400
174
175 CATCAATTGT GTACTTGTA ATGGTCCATT CTCGTCTTGA TATACCCCTT GTTGACATAAA 2460
176
177 CATTAAGTTA TTGCTTCTTG AATTGGTTA GTGCGATGTT GTTGACCCAG CTGATGTGCT 2520
178
179 TAAGATAGTA ACAACAGTTG CTAGAGCTC 2549
180
181
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(2) INFORMATION FOR SEQ ID NO:3:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 492 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 1..15

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 101..218

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

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203 GAG CTC TCC TGG AAG GTAAGTGTGA ATTTGATAAT TTGCGTAGGT ACTTCAGTTT 55
204 Glu Leu Ser Trp Lys
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205      1      5
206
207 GTTGTTCTCG TCAGCACTGA TGGATTCCAA CTGGTGTCT TGCAG GAA CCT GCC      109
208                               Glu Pro Ala
209                               1
210
211 AAG AAA TGG GAG ACA TTG CTA TTG GGC TTA GGA GCT TCT GGC AGT GAA      157
212 Lys Lys Trp Glu Thr Leu Leu Leu Gly Leu Gly Ala Ser Gly Ser Glu
213      5      10      15
214
215 CCC GGT GTT GAA GGG GAA GAA ATC GCT CCA CTT GCC AAG GAA AAT GTA      205
216 Pro Gly Val Glu Gly Glu Glu Ile Ala Pro Leu Ala Lys Glu Asn Val
217      20      25      30      35
218
219 GCC ACT CCT TAAATGAGCT TTGGTTATCC TTGTTTCAAC AATAAGATCA      254
220 Ala Thr Pro *
221
222
223 TTAAGCAAAC GTATTTACTA GCGAACTATG TAGAACCCCTA TTATGGGGTC TCAATCATCT      314
224
225 ACAAAAATGAT TGGTTTTTGC TGGGGAGCAG CAGCATATAA GGCTGTAAAA TCCTGGTTAA      374
226
227 TGTTTTTGTA GGTAAGGGCT ATTTAAGGTG GTGTGGATCA AAGTCAATAG AAAATAGTTA      434
228
229 TTACTAACGT TTGCAACTAA ATACTTAGTA ATGTAGCATA AATAATACTA GAACTAGT      492
230
231
232 (2) INFORMATION FOR SEQ ID NO:4:
233
234 (i) SEQUENCE CHARACTERISTICS:
235 (A) LENGTH: 987 base pairs
236 (B) TYPE: nucleic acid
237 (C) STRANDEDNESS: single
238 (D) TOPOLOGY: linear
239
240 (ii) MOLECULE TYPE: DNA (genomic)
241
242 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:
243
244 AAGCTTTAAC GAGATAGAAA ATTATGTTAC TCCGTTTTGT TCATTACTTA ACAAATGCAA      60
245
246 CAGTATCTTG TACCAAATCC TTTCTCTCTT TTCAAACCTT TCTATTTGGC TGTTGACGGA      120
247
248 GTAATCAGGA TACAAACCAC AAGTATTTAA TTGACTCCTC CGCCAGATAT TATGATTTAT      180
249
250 GAATCCTCGA AAAGCCTATC CATTAAGTCC TCATCTATGG ATATACTTGA CAGTATCTTC      240
251
252 CTGTTTGGGT ATTTTTTTTT CCTGCCAAGT GGAACGGAGA CATGTTATGA TGTATACGGG      300
253
254 AAGCTCGTTA AAAAAAATA CAATAGGAAG AAATGTAACA AACATTGAAT GTTGTTTTTA      360
255

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256 ACCATCCTTC CTTTAGCAGT GTATCAATTT TGTAATAGAA CCATGCATCT CAATCTTAAT 420
257
258 ACTAAAATGC AACTTAATAT AGGCTAAACC AAGATAAAGT AATGTATTCA ACCTTTAGAA 480
259
260 TTGTGCATTC ATAATTAGAT CTTGTTTGTC GTAAAAAATT AGAAAATATA TTTACAGTAA 540
261
262 TTTGGAATAC AAAGCTAAGG GGGGAAGTAAC TAATATTCTA GTGGAGGGAG GGACCAGTAC 600
263
264 CAGTACCTAG ATATTATTTT TAATTACTAT AATAATAATT TAATTAACAC GAGACATAGG 660
265
266 AATGTCAAGT GGTAGCGTAG GAGGGAGTTG GTTTAGTTTT TTAGATACTA GGAGACAGAA 720
267
268 CCGGACGGCC CATTGCAAGG CCAAGTTGAA GTCCAGCCGT GAATCAACAA AGAGAGGGCC 780
269
270 CATAATACTG TCGATGAGCA TTTCCCTATA ATACAGTGTC CACAGTTGCC TTCTGCTAAG 840
271
272 GGATAGCCAC CCGCTATTCT CTTGACACGT GTCAGTAAA CCTGCTACAA ATAAGGCAGG 900
273
274 CACCTCCTCA TTCTCACTCA CTCCTCACA CAGCTCAACA AGTGGTAACT TTTACTCATC 960
275
276 TCCTCCAATT ATTTCTGATT TCATGCA 987
277
278

(2) INFORMATION FOR SEQ ID NO:5:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 4964 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

290
291 AAGCTTTAAC GAGATAGAAA ATTATGTTAC TCCGTTTTGT TCATTACTTA ACAAATGCAA 60
292
293 CAGTATCTTG TACCAAATCC TTTCTCTCTT TTCAAACCTT TCTATTTGGC TGTGACGGA 120
294
295 GTAATCAGGA TACAAACCAC AAGTATTTAA TTGACTCCTC CGCCAGATAT TATGATTTAT 180
296
297 GAATCCTCGA AAAGCCTATC CATTAAGTCC TCATCTATGG ATATACTTGA CAGTATCTTC 240
298
299 CTGTTTGGGT ATTTTTTTTTT CCTGCCAAGT GGAACGGAGA CATGTTATGA TGTATACGGG 300
300
301 AAGCTCGTTA AAAAAAATA CAATAGGAAG AAATGTAACA AACATTGAAT GTTGTTTTTTA 360
302
303 ACCATCCTTC CTTTAGCAGT GTATCAATTT TGTAATAGAA CCATGCATCT CAATCTTAAT 420
304
305 ACTAAAATGC AACTTAATAT AGGCTAAACC AAGATAAAGT AATGTATTCA ACCTTTAGAA 480
306

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307	TTGTGCATTC	ATAATTAGAT	CTTGTTTGTG	GTAAAAAATT	AGAAAAATATA	TTTACAGTAA	540
308							
309	TTTGGAATAC	AAAGCTAAGG	GGGAAGTAAC	TAATATTCTA	GTGGAGGGAG	GGACCAGTAC	600
310							
311	CAGTACCTAG	ATATTATTTT	TAATTACTAT	AATAATAATT	TAATTAAACAC	GAGACATAGG	660
312							
313	AATGTCAAGT	GGTAGCGTAG	GAGGGAGTTG	GTTTAGTTTT	TTAGATACTA	GGAGACAGAA	720
314							
315	CCGACGGCC	CATTGCAAGG	CCAAGTTGAA	GTCCAGCCGT	GAATCAACAA	AGAGAGGGCC	780
316							
317	CATAATACTG	TCGATGAGCA	TTTCCCTATA	ATACAGTGTC	CACAGTTGCC	TTCTGCTAAG	840
318							
319	GGATAGCCAC	CCGCTATTCT	CTTGACACGT	GTCAGTGAAA	CCTGCTACAA	ATAAGGCAGG	900
320							
321	CACCTCCTCA	TTCTCACTCA	CTCACTCACA	CAGCTCAACA	AGTGGTAACT	TTTACTCATC	960
322							
323	TCCTCCAATT	ATTTCTGATT	TCATGCATGT	TTCCCTACAT	TCTATTATGA	ATCGTGTGTG	1020
324							
325	GGTGATAAAA	CGTTGTTTCA	TATCTCATCT	CATCTATTCT	GATTTTGATT	CTCTTGCCTA	1080
326							
327	CTGTAATCGG	TGATAAATGT	GAATGCTTCC	TTTCTTCTCA	GAAATCAATT	TCTGTTTTGT	1140
328							
329	TTTTGTTCAT	CTGTAGCTTA	TTCTCTGGTA	GATTCCCCTT	TTTGTAGACC	ACACATCACA	1200
330							
331	TGGCAAGCAT	CACAGCTTCA	CACCACTTTG	TGTCAAGAAG	CCAAACTTCA	CTAGACACCA	1260
332							
333	AATCAACCTT	GTCACAGATA	GGACTCAGGA	ACCATACTCT	GACTCACAAT	GGTTTAAGGG	1320
334							
335	CTGTTAACAA	GCTTGATGGG	CTCCAATCAA	CAACTAATAC	TAAGGTAACA	CCCAAGATGG	1380
336							
337	CATCCAGAAC	TGAGACCAAG	AGACCTGGAT	GCTCAGCTAC	CATTGTTTGT	GGAAAGGGAA	1440
338							
339	TGAACTTGAT	CTTTGTGGGT	ACTGAGGTTG	GTCCTTGGAG	CAAACTGGT	GGACTAGGTG	1500
340							
341	ATGTTCTTGG	TGGACTACCA	CCAGCCCCTG	CAGTAAGTCT	TTCTTTCATT	TGGTTACCTA	1560
342							
343	CTCATTCATT	ACTTATTTTG	TTTAGTTAGT	TTCTACTGCA	TCAGTCTTTT	TATCATTTAG	1620
344							
345	GCCCCGCGGAC	AGCGGGTAAT	GACAATATCC	CCCCGTTATG	ACCAATACAA	AGATGCTTGG	1680
346							
347	GATACTGGCG	TTGCGGTTGA	GGTACATCTT	CCTATATTGA	TACGGTACAA	TATTGTTCTC	1740
348							
349	TTACATTTCC	TGATTCAAGA	ATGTGATCAT	CTGCAGGTCA	AAGTTGGAGA	CAGCATTGAA	1800
350							
351	ATTGTTTCGTT	TCTTTCCTG	CTATAAACGT	GGGGTTGATC	GTGTTTTTGT	TGACCACCCA	1860
352							
353	ATGTTCTTGG	AGAAAGTAAG	CATATTATGA	TTATGAATCC	GTCCTGAGGG	ATACGCAGAA	1920
354							
355	CAGGTCATTT	TGAGTATCTT	TTAACTCTAC	TGGTGCTTTT	ACTCTTTTAA	GGTTTGGGGC	1980
356							
357	AAAACTGGTT	CAAAAATCTA	TGGCCCCAAA	GCTGGACTAG	ATTATCTGGA	CAATGAACTT	2040

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358									
359	AGGTTTCAGCT	TGTTGTGTCA	AGTAAGTTAG	TTACTCTTGA	TTTTTATGTG	GCATTTTACT		2100	
360									
361	CTTTTGTCTT	TAATCGTTTT	TTTAACCTTG	TTTCTCAGG	CAGCCCTAGA	GGCACCTAAA		2160	
362									
363	GTTTTGAATT	TGAACAGTAG	CAACTACTTC	TCAGGACCAT	ATGGTAATTA	ACACATCCTA		2220	
364									
365	GTTTCAGAAA	ACTCCTTACT	ATATCATTGT	AGGTAATCAT	CTTTATTTTG	CCTATTCCTG		2280	
366									
367	CAGGAGAGGA	TGTTCTCTTC	ATTGCCAATG	ATTGGCACAC	AGCTCTCATT	CCTTGCTACT		2340	
368									
369	TGAAGTCAAT	GTACCAGTCC	AGAGGAATCT	ACTTGAATGC	CAAGGTAAAA	TTTCTTTGTA		2400	
370									
371	TTCACTCGAT	TGCACGTTAC	CCTGCAAATC	AGTAAGGTTG	TATTAATATA	TGATAAATTT		2460	
372									
373	CACATTGCCT	CCAGGTTGCT	TTCTGCATCC	ATAACATTGC	CTACCAAGGT	CGATTTTCTT		2520	
374									
375	TCTCTGACTT	CCCTCTTCTC	AATCTTCCTG	ATGAATTCAG	GGGTTCTTTT	GATTTTCATTG		2580	
376									
377	ATGGGTATGT	ATTTATGCTT	GAAATCAGAC	CTCCAACTTT	TGAAGCTCTT	TTGATGCTAG		2640	
378									
379	TAAATTGAGT	TTTTAAAAAT	TTGCAGATAT	GAGAAGCCTG	TTAAGGGTAG	GAAAATCAAC		2700	
380									
381	TGGATGAAGG	CTGGGATATT	AGAATCACAT	AGGGTGGTTA	CAGTGAGCCC	ATACTATGCC		2760	
382									
383	CAAGAACTTG	TCTCTGCTGT	TGACAAGGGA	GTTGAATTGG	ACAGTGTCTT	TCGTAAGACT		2820	
384									
385	TGCATAACTG	GGATTGTGAA	TGGCATGGAT	ACACAAGAGT	GGAACCCAGC	GA CTGACAAA		2880	
386									
387	TACACAGATG	TCAAATACGA	TATAACCACT	GTAAGATAAG	ATTTTTCCGA	CTCCAGTATA		2940	
388									
389	TACTAAATTA	TTTTGTATGT	TTATGAAATT	AAAGAGTTCT	TGCTAATCAA	AATCTCTATA		3000	
390									
391	CAGGTCATGG	ACGCAAAACC	TTTACTAAAG	GAGGCTCTTC	AAGCAGCAGT	TGGCTTGCCT		3060	
392									
393	GTTGACAAGA	AGATCCCTTT	GATTGGCTTC	ATCGGCAGAC	TTGAGGAGCA	GAAAGGTTCA		3120	
394									
395	GATATTCTTG	TTGCTGCAAT	TCACAAGTTC	ATCGGATTGG	ATGTTCAAAT	TGTAGTCCTT		3180	
396									
397	GTAAGTACCA	AATGGACTCA	TGGTATCTCT	CTTGTTGAGT	TTACTTGTGC	CGAAACTGAA		3240	
398									
399	ATTGACCTGC	TACTCATCCT	ATGCATCAGG	GA ACTGGCAA	AAAGGATTTT	GAGCAGGAGA		3300	
400									
401	TTGAACAGCT	CGAAGTGTTG	TACCCTAACA	AAGCTAAAGG	AGTGGCAAAA	TTCAATGTCC		3360	
402									
403	CTTTGGCTCA	CATGATCACT	GCTGGTGCTG	ATTTTATGTT	GGTTCCAAGC	AGATTTGAAC		3420	
404									
405	CTTGTGGTCT	CATTCACTTA	CATGCTATGC	GATATGGAAC	AGTAAGAACC	AGAAGAGCTT		3480	
406									
407	GTACCTTTTT	ACTGAGTTTT	TAAAAAAGA	ATCATAAGAC	CTTGTTTTCC	ATCTAAAGTT		3540	
408									

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409	TAATAACCAA	CTAAATGTTA	CTGCAGCAAG	CTTTTCATTT	CTGAAAATTG	GTTATCTGAT	3600
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411	TTTAACGTAA	TCACATGTGA	GTCAGGTACC	AATCTGTGCA	TCGACTGGTG	GACTTGTTGA	3660
412							
413	CACTGTGAAA	GAAGGCTATA	CTGGATTCCA	TATGGGAGCC	TTCAATGTTG	AAGTATGTGA	3720
414							
415	TTTTACATCA	ATTGTGTACT	TGTACATGGT	CCATTCTCGT	CTTGATATAC	CCCTTGTTGC	3780
416							
417	ATAAACATTA	ACTTATTGCT	TCTTGAATTT	GGTTAGTGCG	ATGTTGTTGA	CCCAGCTGAT	3840
418							
419	GTGCTTAAGA	TAGTAACAAC	AGTTGCTAGA	GCTCTTGCAG	TCTATGGCAC	CCTCGCATTT	3900
420							
421	GCTGAGATGA	TAAAAAATTG	CATGTCAGAG	GAGCTCTCCT	GGAAGGTAAG	TGTGAATTTG	3960
422							
423	ATAATTTGCG	TAGGTACTTC	AGTTTGTGTG	TCTCGTCAGC	ACTGATGGAT	TCCAACGGT	4020
424							
425	GTTCTTGCG	GAACCTGCCA	AGAAATGGGA	GACATTGCTA	TTGGGCTTAG	GAGCTTCTGG	4080
426							
427	CAGTGAACCC	GGTGTGAAG	GGGAAGAAAT	CGCTCCACTT	GCCAAGGAAA	ATGTAGCCAC	4140
428							
429	TCCTTAAATG	AGCTTTGGTT	ATCCTTGTTT	CAACAATAAG	ATCATTAAGC	AAACGTATTT	4200
430							
431	ACTAGCGAAC	TATGTAGAAC	CCTATTATGG	GGTCTCAATC	ATCTACAAAA	TGATTGGTTT	4260
432							
433	TTGCTGGGGA	GCAGCAGCAT	ATAAGGCTGT	AAAATCCTGG	TTAATGTTTT	TGTAGGTAAG	4320
434							
435	GGCTATTTAA	GGTGGTGTGG	ATCAAAGTCA	ATAGAAAATA	GTTATTACTA	ACGTTTGCAA	4380
436							
437	CTAAATACTT	AGTAATGTAG	CATAAATAAT	ACTAGAACTA	GTAGCTAATA	TATATGCGTG	4440
438							
439	AATTTGTTGT	ACCTTTTCTT	GCATAATTAT	TTGCAGTACA	TATATAATGA	AAATTACCCA	4500
440							
441	AGGAATCAAT	GTTTCTTGCT	CCGTCCTCCT	TTGATGATTT	TTTACGCAAT	ACAGAGCTAG	4560
442							
443	TGTGTTATGT	TATAAATTTT	GTTTAAAAGA	AGTAATCAAA	TTCAAATTAG	TTGTTTGGTC	4620
444							
445	ATATGAAAGA	AGCTGCCAGG	CTAACTTTGA	GGAGATGGCT	ATTGAATTTT	AAAATGATTA	4680
446							
447	TGTGAAAACA	ATGCAACATC	TATGTCAATC	AACACTTAAA	TTATTGCATT	TAGAAAGATA	4740
448							
449	TTTTTGAGCC	CATGACACAT	TCATTCTATA	AGTAAGGTAG	TATGTATGAT	TGAATGGACT	4800
450							
451	ACAGCTCAAT	CAAAGCATCT	CCTTTACATA	ACGGCACTGT	CTCTTGTCTA	CTACTCTATT	4860
452							
453	GGTAGTAGTA	GTAGTAATTT	TACAATCCAA	ATTGAATAGT	AATAAGATGC	TCTCTATTTA	4920
454							
455	CTAAAGTAGT	AGTATTATTC	TTTCGTTACT	CTAAAGCAAC	AAAA		4964
456							
457							
458	(2)	INFORMATION	FOR	SEQ	ID	NO:6:	
459							

RAW SEQUENCE LISTING
PATENT APPLICATION US/08/070,455DATE: 12/10/93
TIME: 12:00:38

INPUT SET: S2078.raw

460 (i) SEQUENCE CHARACTERISTICS:
461 (A) LENGTH: 69 amino acids
462 (B) TYPE: amino acid
463 (C) STRANDEDNESS: single
464 (D) TOPOLOGY: linear
465
466 (ii) MOLECULE TYPE: peptide
467
468 (ix) FEATURE:
469 (A) NAME/KEY: Modified-site
470 (B) LOCATION: 1..69
471 (D) OTHER INFORMATION: /note= "Amino acid sequence encoded
472 by nucleotides 1-207 of SEQ ID NO. 2."
473
474
475 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:
476
477 Asn Lys Leu Asp Gly Leu Gln Ser Thr Thr Asn Thr Lys Val Thr Pro
478 1 5 10 15
479
480 Lys Met Ala Ser Arg Thr Glu Thr Lys Arg Pro Gly Cys Ser Ala Thr
481 20 25 30
482
483 Ile Val Cys Gly Lys Gly Met Asn Leu Ile Phe Val Gly Thr Glu Val
484 35 40 45
485
486 Gly Pro Trp Ser Lys Thr Gly Gly Leu Gly Asp Val Leu Gly Gly Leu
487 50 55 60
488
489 Pro Pro Ala Leu Ala
490 65
491
492
493 (2) INFORMATION FOR SEQ ID NO:7:
494
495 (i) SEQUENCE CHARACTERISTICS:
496 (A) LENGTH: 27 amino acids
497 (B) TYPE: amino acid
498 (C) STRANDEDNESS: single
499 (D) TOPOLOGY: linear
500
501 (ii) MOLECULE TYPE: peptide
502
503 (ix) FEATURE:
504 (A) NAME/KEY: Modified-site
505 (B) LOCATION: 1..27
506 (D) OTHER INFORMATION: /note= "Amino acid sequence encoded
507 by nucleotides 296-377 of SEQ ID NO. 2."
508
509 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:
510

320

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RAW SEQUENCE LISTING
PATENT APPLICATION US/08/070,455DATE: 12/10/93
TIME: 12:00:48

INPUT SET: S2078.raw

511 Ala Arg Gly His Arg Val Met Thr Ile Ser Pro Arg Tyr Asp Gln Tyr
512 1 5 10 15
513
514 Lys Asp Ala Trp Asp Thr Gly Val Ala Val Glu
515 20 25
516
517

(2) INFORMATION FOR SEQ ID NO:8:

518
519
520 (i) SEQUENCE CHARACTERISTICS:
521 (A) LENGTH: 33 amino acids
522 (B) TYPE: amino acid
523 (C) STRANDEDNESS: single
524 (D) TOPOLOGY: linear
525
526 (ii) MOLECULE TYPE: peptide
527
528 (ix) FEATURE:
529 (A) NAME/KEY: Modified-site
530 (B) LOCATION: 1..33
531 (D) OTHER INFORMATION: /note= "Amino acid sequence encoded
532 by nucleotides 452-550 of SEQ ID NO. 2."
533
534 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:
535
536 Val Lys Val Gly Asp Ser Ile Glu Ile Val Arg Phe Phe His Cys Tyr
537 1 5 10 15
538
539 Lys Arg Gly Val Asp Arg Val Phe Val Asp His Pro Met Phe Leu Glu
540 20 25 30
541
542 Lys
543
544

(2) INFORMATION FOR SEQ ID NO:9:

545
546
547 (i) SEQUENCE CHARACTERISTICS:
548 (A) LENGTH: 30 amino acids
549 (B) TYPE: amino acid
550 (C) STRANDEDNESS: single
551 (D) TOPOLOGY: linear
552
553 (ii) MOLECULE TYPE: peptide
554
555 (ix) FEATURE:
556 (A) NAME/KEY: Modified-site
557 (B) LOCATION: 1..30
558 (D) OTHER INFORMATION: /note= "Amino acid sequence encoded
559 by nucleotides 647-736 of SEQ ID NO. 2."
560
561 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:

321

R74

RAW SEQUENCE LISTING
PATENT APPLICATION US/08/070,455DATE: 12/10/93
TIME: 12:00:59

INPUT SET: S2078.raw

562
563 Val Trp Gly Lys Thr Gly Ser Lys Ile Tyr Gly Pro Lys Ala Gly Leu
564 1 5 10 15
565
566 Asp Tyr Leu Asp Asn Glu Leu Arg Phe Ser Leu Leu Cys Gln
567 20 25 30
568
569

570 (2) INFORMATION FOR SEQ ID NO:10:

571
572 (i) SEQUENCE CHARACTERISTICS:
573 (A) LENGTH: 21 amino acids
574 (B) TYPE: amino acid
575 (C) STRANDEDNESS: single
576 (D) TOPOLOGY: linear
577
578 (ii) MOLECULE TYPE: peptide
579
580 (ix) FEATURE:
581 (A) NAME/KEY: Modified-site
582 (B) LOCATION: 1..21
583 (D) OTHER INFORMATION: /note= "Amino acid sequence encoded
584 by nucleotides 815-878 of SEQ ID NO. 2."
585

586 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:10:

587
588 Ala Ala Leu Glu Ala Pro Lys Val Leu Asn Leu Asn Ser Ser Asn Tyr
589 1 5 10 15
590
591 Phe Ser Gly Pro Tyr
592 20
593
594

595 (2) INFORMATION FOR SEQ ID NO:11:

596
597 (i) SEQUENCE CHARACTERISTICS:
598 (A) LENGTH: 34 amino acids
599 (B) TYPE: amino acid
600 (C) STRANDEDNESS: single
601 (D) TOPOLOGY: linear
602
603 (ii) MOLECULE TYPE: peptide
604
605 (ix) FEATURE:
606 (A) NAME/KEY: Modified-site
607 (B) LOCATION: 1..34
608 (D) OTHER INFORMATION: /note= "Amino acid sequence encoded
609 by nucleotides 878 and 959-1059 of SEQ ID NO. 2."
610
611 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:11:
612

322

875

RAW SEQUENCE LISTING
PATENT APPLICATION US/08/070,455DATE: 12/10/93
TIME: 12:01:10

INPUT SET: S2078.raw

613 Gly Glu Asp Val Leu Phe Ile Ala Asn Asp Trp His Thr Ala Leu Ile
614 1 5 10 15
615
616 Pro Cys Tyr Leu Lys Ser Met Tyr Gln Ser Arg Gly Ile Tyr Leu Asn
617 20 25 30
618
619 Ala Lys
620
621

(2) INFORMATION FOR SEQ ID NO:12:

622
623
624 (i) SEQUENCE CHARACTERISTICS:
625 (A) LENGTH: 38 amino acids
626 (B) TYPE: amino acid
627 (C) STRANDEDNESS: single
628 (D) TOPOLOGY: linear
629
630 (ii) MOLECULE TYPE: peptide
631
632 (ix) FEATURE:
633 (A) NAME/KEY: Modified-site
634 (B) LOCATION: 1..38
635 (D) OTHER INFORMATION: /note= "Amino acid sequence encoded
636 by nucleotides 1150-1263 of SEQ ID NO 2."
637
638 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:12:
639
640 Val Ala Phe Cys Ile His Asn Ile Ala Tyr Gln Gly Arg Phe Ser Phe
641 1 5 10 15
642
643 Ser Asp Phe Pro Leu Leu Asn Leu Pro Asp Glu Phe Arg Gly Ser Phe
644 20 25 30
645
646 Asp Phe Ile Asp Gly Tyr
647 35
648
649

(2) INFORMATION FOR SEQ ID NO:13:

650
651
652 (i) SEQUENCE CHARACTERISTICS:
653 (A) LENGTH: 79 amino acids
654 (B) TYPE: amino acid
655 (C) STRANDEDNESS: single
656 (D) TOPOLOGY: linear
657
658 (ii) MOLECULE TYPE: peptide
659
660 (ix) FEATURE:
661 (A) NAME/KEY: Modified-site
662 (B) LOCATION: 1..79
663 (D) OTHER INFORMATION: /note= "Amino acid sequence encoded

RAW SEQUENCE LISTING PATENT APPLICATION US/08/070,455

DATE: 12/10/93
TIME: 12:01:21

INPUT SET: S2078.raw

664 by nucleotides 1349-1585 of SEQ ID NO 2."
665
666 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:13:
667
668 Lys Pro Val Lys Gly Arg Lys Ile Asn Trp Met Lys Ala Gly Ile Leu
669 1 5 10 15
670
671 Glu Ser His Arg Val Val Thr Val Ser Pro Tyr Tyr Ala Gln Glu Leu
672 20 25 30
673
674 Val Ser Ala Val Asp Lys Gly Val Glu Leu Asp Ser Val Leu Arg Lys
675 35 40 45
676
677 Thr Cys Ile Thr Gly Ile Val Asn Gly Met Asp Thr Gln Glu Trp Asn
678 50 55 60
679
680 Pro Ala Thr Asp Lys Tyr Thr Asp Val Lys Tyr Asp Ile Thr Thr
681 65 70 75
682
683
684 (2) INFORMATION FOR SEQ ID NO:14:
685
686 (i) SEQUENCE CHARACTERISTICS:
687 (A) LENGTH: 59 amino acids
688 (B) TYPE: amino acid
689 (C) STRANDEDNESS: single
690 (D) TOPOLOGY: linear
691
692 (ii) MOLECULE TYPE: peptide
693
694 (ix) FEATURE:
695 (A) NAME/KEY: Modified-site
696 (B) LOCATION: 1..59
697 (D) OTHER INFORMATION: /note= "Amino acid sequence encoded
698 by nucleotides 1676-1855 of SEQ ID NO 2."
699
700 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:14:
701
702 Val Met Asp Ala Lys Pro Leu Leu Lys Glu Ala Leu Gln Ala Ala Val
703 1 5 10 15
704
705 Gly Leu Pro Val Asp Lys Lys Ile Pro Leu Ile Gly Phe Ile Gly Arg
706 20 25 30
707
708 Leu Glu Glu Gln Lys Gly Ser Asp Ile Leu Ala Val Ala Ile His Lys
709 35 40 45
710
711 Phe Ile Gly Leu Asp Val Gln Ile Val Val Leu
712 50 55
713
714

RAW SEQUENCE LISTING
PATENT APPLICATION US/08/070,455DATE: 12/10/93
TIME: 12:01:32

INPUT SET: S2078.raw

715 (2) INFORMATION FOR SEQ ID NO:15:

716

717 (i) SEQUENCE CHARACTERISTICS:

718 (A) LENGTH: 64 amino acids

719 (B) TYPE: amino acid

720 (C) STRANDEDNESS: single

721 (D) TOPOLOGY: linear

722

723 (ii) MOLECULE TYPE: peptide

724

725 (ix) FEATURE:

726 (A) NAME/KEY: Modified-site

727 (B) LOCATION: 1..64

728 (D) OTHER INFORMATION: /note= "Amino acid sequence encoded
729 by nucleotides 1945-2136 of SEQ ID NO 2."

730

731 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:15:

732

733 Gly Thr Gly Lys Lys Glu Phe Glu Gln Glu Ile Glu Gln Leu Glu Val
734 1 5 10 15

735

736 Leu Tyr Pro Asn Lys Ala Lys Gly Val Ala Lys Phe Asn Val Pro Leu
737 20 25 30

738

739 Ala His Met Ile Thr Ala Gly Ala Asp Phe Met Leu Val Pro Ser Arg
740 35 40 45

741

742 Phe Glu Pro Cys Gly Leu Ile Gln Leu His Ala Met Arg Tyr Gly Thr
743 50 55 60

744

745

746 (2) INFORMATION FOR SEQ ID NO:16:

747

748 (i) SEQUENCE CHARACTERISTICS:

749 (A) LENGTH: 29 amino acids

750 (B) TYPE: amino acid

751 (C) STRANDEDNESS: single

752 (D) TOPOLOGY: linear

753

754 (ii) MOLECULE TYPE: peptide

755

756 (ix) FEATURE:

757 (A) NAME/KEY: Modified-site

758 (B) LOCATION: 1..29

759 (D) OTHER INFORMATION: /note= "Amino acid sequence encoded
760 by nucleotides 2301-2386 of SEQ ID NO 2."

761

762 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:16:

763

764 Val Pro Ile Cys Ala Ser Thr Gly Gly Leu Val Asp Thr Val Lys Glu
765 1 5 10 15

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RAW SEQUENCE LISTING
PATENT APPLICATION US/08/070,455DATE: 12/10/93
TIME: 12:01:43

INPUT SET: S2078.raw

766
767 Gly Tyr Thr Gly Phe His Met Gly Ala Phe Asn Val Glu
768 20 25
769
770
771 (2) INFORMATION FOR SEQ ID NO:17:
772
773 (i) SEQUENCE CHARACTERISTICS:
774 (A) LENGTH: 19 amino acids
775 (B) TYPE: amino acid
776 (C) STRANDEDNESS: single
777 (D) TOPOLOGY: linear
778
779 (ii) MOLECULE TYPE: peptide
780
781 (ix) FEATURE:
782 (A) NAME/KEY: Modified-site
783 (B) LOCATION: 1..19
784 (D) OTHER INFORMATION: /note= "Amino acid sequence encoded
785 by nucleotides 2492-2459 of SEQ ID NO 2."
786
787 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:17:
788
789 Cys Asp Val Val Asp Pro Ala Asp Val Leu Lys Ile Val Thr Thr Val
790 1 5 10 15
791
792 Ala Arg Ala
793
794
795 (2) INFORMATION FOR SEQ ID NO:18:
796
797 (i) SEQUENCE CHARACTERISTICS:
798 (A) LENGTH: 111 amino acids
799 (B) TYPE: amino acid
800 (C) STRANDEDNESS: single
801 (D) TOPOLOGY: linear
802
803 (ii) MOLECULE TYPE: peptide
804
805 (ix) FEATURE:
806 (A) NAME/KEY: Modified-site
807 (B) LOCATION: 1..111
808 (D) OTHER INFORMATION: /note= "Amino acid sequence encoded
809 by nucleotides 1200-1532 of SEQ ID NO 5."
810
811 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:18:
812
813 Met Ala Ser Ile Thr Ala Ser His His Phe Val Ser Arg Ser Gln Thr
814 1 5 10 15
815
816 Ser Leu Asp Thr Lys Ser Thr Leu Ser Gln Ile Gly Leu Arg Asn His

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RAW SEQUENCE LISTING PATENT APPLICATION US/08/070,455

DATE: 12/10/93
TIME: 12:01:54

INPUT SET: S2078.raw

```

817          20          25          30
818
819  Thr Leu Thr His Asn Gly Leu Arg Ala Val Asn Lys Leu Asp Gly Leu
820          35          40          45
821
822  Gln Ser Thr Thr Asn Thr Lys Val Thr Pro Lys Met Ala Ser Arg Thr
823          50          55          60
824
825  Glu Thr Lys Arg Pro Gly Cys Ser Ala Thr Ile Val Cys Gly Lys Gly
826          65          70          75          80
827
828  Met Asn Leu Ile Phe Val Gly Thr Glu Val Gly Pro Trp Ser Lys Thr
829          85          90          95
830
831  Gly Gly Leu Gly Asp Val Leu Gly Gly Leu Pro Pro Ala Leu Ala
832          100          105          110
833
834

```

(2) INFORMATION FOR SEQ ID NO:19:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 43 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 1..43
- (D) OTHER INFORMATION: /note= "Amino acid sequence encoded by nucleotides 3817-3945 of SEQ ID NO. 5."

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:19:

```

853  Cys Asp Val Val Asp Pro Ala Asp Val Leu Lys Ile Val Thr Thr Val
854  1          5          10          15
855
856  Ala Arg Ala Leu Ala Val Tyr Gly Thr Leu Ala Phe Ala Glu Met Ile
857          20          25          30
858
859  Lys Asn Cys Met Ser Glu Glu Leu Ser Trp Lys
860          35          40
861

```

(2) INFORMATION FOR SEQ ID NO:20:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 38 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single

RAW SEQUENCE LISTING
PATENT APPLICATION US/08/070,455DATE: 12/10/93
TIME: 12:02:05

INPUT SET: S2078.raw

868 (D) TOPOLOGY: linear
869
870 (ii) MOLECULE TYPE: peptide
871
872 (ix) FEATURE:
873 (A) NAME/KEY: Modified-site
874 (B) LOCATION: 1..38
875 (D) OTHER INFORMATION: /note= "Amino acid sequence encoded
876 by nucleotides 4031-4144 of SEQ ID NO. 5."
877
878 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:20:
879
880 Glu Pro Ala Lys Lys Trp Glu Thr Leu Leu Leu Gly Leu Gly Ala Ser
881 1 5 10 15
882
883 Gly Ser Glu Pro Gly Val Glu Gly Glu Glu Ile Ala Pro Leu Ala Lys
884 20 25 30
885
886 Glu Asn Val Ala Thr Pro
887 35
888
889
890 (2) INFORMATION FOR SEQ ID NO:21:
891
892 (i) SEQUENCE CHARACTERISTICS:
893 (A) LENGTH: 17 base pairs
894 (B) TYPE: nucleic acid
895 (C) STRANDEDNESS: single
896 (D) TOPOLOGY: linear
897
898 (ii) MOLECULE TYPE: RNA
899
900 (ix) FEATURE:
901 (A) NAME/KEY: misc_RNA
902 (B) LOCATION: 1
903 (D) OTHER INFORMATION: /note= "Nucleotide 1 is a 7-methyl
904 guanine added by 5'-5' linkage as an RNA cap."
905
906 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:21:
907
908 GAUGGCAAGA AAAAAAA
909

17

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R81

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SEQUENCE VERIFICATION REPORT
PATENT APPLICATION US/08/070,455

DATE: 12/10/93
TIME: 12:02:14

INPUT SET: S2078.raw

Line	Error	Original Text
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SEQUENCE MISSING ITEM REPORT
PATENT APPLICATION US/08/070,455

DATE: 12/10/93
TIME: 12:02:15

INPUT SET: S2078.raw

APPLICATION NUMBER
FILING DATE
PRIOR APPLICATION DATA

330

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PAGE: 1

SEQUENCE CORRECTION REPORT
PATENT APPLICATION US/08/070,455

DATE: 12/10/93
TIME: 12:02:15

INPUT SET: S2078.raw

Line	Original Text	Corrected Text
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